

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/7/6,964

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

BEST AVAILABLE COPY

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000
 TIME: 07:50:03

Input Set : A:\R10301.app
 Output Set: N:\CRF3\12072000\I716964.raw

Does Not Comply
 Corrected Diskette Needed

P.6

```

3 <110> APPLICANT: O'Donnell, Michael E.
4     Yuzhakov, Alexander
5     Yurieva, Olga
6     Jeruzalmi, David
7     Bruck, Irina
8     Kuriyan, John
10 <120> TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
11     FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
12     USE THEREOF
14 <130> FILE REFERENCE: 22221/1030
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/716,964
C--> 17 <141> CURRENT FILING DATE: 2000-11-21
19 <150> PRIOR APPLICATION NUMBER: 60/143,202
20 <151> PRIOR FILING DATE: 1997-04-08
22 <150> PRIOR APPLICATION NUMBER: 08/823,407
23 <151> PRIOR FILING DATE: 1997-04-08
25 <150> PRIOR APPLICATION NUMBER: 09/057,416
26 <151> PRIOR FILING DATE: 1998-04-08
28 <160> NUMBER OF SEQ ID NOS: 212
30 <170> SOFTWARE: PatentIn Ver. 2.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 2007
34 <212> TYPE: DNA
35 <213> ORGANISM: Thermus thermophilus
37 <400> SEQUENCE: 1
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39 gccacctct ccaggggggc caaggcgtgc aaggagagga acgtccgcac cagccctat 120
40 actagcctt tgagcgccct ctaccgccc ttccgcccc tcacctcca ggaggtgtg 180
41 gggcaggagc acgtgaagga gccctctctc aaggccatcc gggaggggag gctcgccag 240
42 gctacctct tctccgggcc caggggcgtg ggcaagacca ccacggcgag gctcctcgcc 300
43 atggcggttg ggtgccagg ggaagacccc ccttgccggg tctgccccta ctgccaggc 360
44 gtgcagaggg gcgccccccc ggacgtgtg gacattgacg ccgccagcaa caactccgtg 420
45 gaggacgtgc gggagctgag ggaaggatc cactcgcgcc cctctctgc cccaggaag 480
46 gtcttcatcc tggacgaggc ccacatctc tccaaaagcg ccttcaacgc cctcctcaag 540
47 accctggagg agcccccgcc ccaagtcctc tctgtcttcg ccaccaccga gcccgaggag 600
48 atgcccccca ccatctctc ccgcacccag cacttccgt tccgcgcct caggaggag 660
49 gagatcgctt ttaagctcg gcgcacctg gaggcgttg ggcgggaggc ggaggaggag 720
50 gccctctctc tctcgcggc cctggcgagc ggggccctta gggacgcga aagcctcctg 780
51 gagcgcttcc tctcctgga aggccccctc acccggaagg aggtggagcg cgccttaggc 840
52 tccccccag ggaacgggtt ggccgagatc gccgcctccc tgcgagggg gaaaacggcg 900
53 gaggcccttg gcctcgcggc gcgcctctac ggggaagggt acgccccgag gacgtgtgc 960
54 tcyggccttt tggaggtgtt ccgggaaggc ctctacgcgc ccttcggcct cgcgggaacc 1020
55 ccccttcccg cccgcgccc ggccctgac gccgccatga ccgcctgga caggccatg 1080
56 ggcgcctcg ccgcgcctc cgacgcctta agcctggagg tggccctcct ggaggcggga 1140
57 agggcccttg ccgcgaggc cctaccccg cccacgggcg ctccttcccc agaggtcggc 1200
58 cccaagccgg aaagccccc gacccggaa ccccaaggc ccgaggaggc gcccgacctg 1260
59 cgggagcgtt ggcgggcctt cctcgaggcc ctcaggcca cctacgggc cttcgtgcgg 1320

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Input Set : A:\R10301.app

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60 gagggccggc cggaggtccg ggaaggccag ctctgcctcg ctttcccca ggacaaggcc 1380
61 ttccactacc gcaaggcctc ggaacagaag gtgaggctcc tccccctggc ccaggcccat 1440
62 ttccgggttg aggaggtcgt cctcgtctcg gagggagaaa aaaaaagcct gagcccaagg 1500
63 ccccgcccg cccacacctc tgaagcgccc gcaccccgcg gccctcccca ggaggagata 1560
64 gagggcgagg aagcggcgga ggaggccccc gagggagcct tgaggcggtt ggtccgcctc 1620
65 ctgggggggc gggtyctcty ggtgcggcgg ccaggaccc ggaggcgcc ggaggaggaa 1680
66 cccctgagcc aagacgagat agggggtact ggtatataat gggggcatga cgcggaccac 1740
67 cgacctcgga caagagaccg tggacaacat cctcaagcgc ctccgcgcta ttgaggccca 1800
68 ggtgcggggg ctccagaaga tggaggccga ggcccgccc tgcgacgag tcccaacca 1860
69 gatgaccgac accaagaagg ccatggaggg ggcggccacc ctgactctcc acgagttcct 1920
70 gaacgtctgc gcgcggagg tctccgagg caaggtgaac ccaagaagc ccgaggagat 1980
71 cggccaccatg ctgaagaact tcattata 2007

```

74 <210> SEQ ID NO: 2

75 <211> LENGTH: 529

76 <212> TYPE: PRF

77 <213> ORGANISM: Thermus thermophilus

79 <400> SEQUENCE: 2

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81   1           5           10           15
83 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
84           20           25           30
86 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
87           35           40           45
89 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
90           50           55           60
92 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
93   65           70           75           80
95 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
96           85           90           95
98 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
99           100          105          110
101 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
102           115          120          125
104 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
105           130          135          140
107 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
108 145           150           155           160
110 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
111           165          170          175
113 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
114           180          185          190
116 Glu Ala Glu Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
117           195          200          205
119 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
120           210          215          220
122 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
123 225           230           235           240
125 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
126           245          250          255

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Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

128 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 129 260 265 270
 131 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 132 275 280 285
 134 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 135 290 295 300
 137 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 138 305 310 315 320
 140 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 141 325 330 335
 143 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 144 340 345 350
 146 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 147 355 360 365
 149 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 150 370 375 380
 152 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 153 385 390 395 400
 155 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 156 405 410 415
 158 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 159 420 425 430
 161 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 162 435 440 445
 164 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 165 450 455 460
 167 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
 168 465 470 475 480
 170 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
 171 485 490 495
 173 Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
 174 500 505 510
 176 Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
 177 515 520 525
 179 Ile
 183 <210> SEQ ID NO: 3
 184 <211> LENGTH: 1590
 185 <212> TYPE: DNA
 186 <213> ORGANISM: Thermus thermophilus
 188 <400> SEQUENCE: 3
 189 gtgagcgccc tctaccgccc ctcccgcccc ctcaccttcc aggaggtggt ggggcaggag 60
 190 cactgaagg agccctccct caaggccatc cgggagggga ggctcgccca gccctacctc 120
 191 ttctccgggc ccaggggcgt gggcaagacc accacggcga ggctcctcgc catggcggtg 180
 192 ggggtgccagg gggaaagacc cctttgcggg gtctgcccc actgccaggc ggtgcagagg 240
 193 ggcgcccacc cggacgtggt ggacattgac gccgccagca acaactccgt ggaggacgtg 300
 194 cgggaqctga gggaaaggat ccacctcgcc cccctctctg cccccaggaa ggtcttcac 360
 195 ctggacgagg cccacatgct ctccaaaagc gccttcaacg ccctcctcaa gacctggag 420
 196 gagccccgc cccacgtcct ctctgtcttc gccaccaccg agcccgagag gatgcccc 480
 197 accatcctct ccgcaccca gcacttcgc ttccgcccgc tcacggagga ggagatcgcc 540

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Input Set : A:\R10301.app
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198 ttttaagctcc ggcgcaccc ggaagcccg gggcgggagg cggaggaggga ggcctctctc 600
199 ctctctgccc gcctggcgga cggggccctt agggacggcg aaagcctctt ggagcgtctc 660
200 ctctctcttg aaggccccc caccggaaag gagggtqagc gcgccttagg ctccccccca 720
201 gggaccgggg tggccgagat cgcgcctcc ctcgcgagg ggaacacggc ggaagccctg 780
202 ggcctgcccc ggcgcctcta cggggaagg taagccccc ggaagcctgt ctcgggctt 840
203 ttggaggtgt tccgggaagg cctctacgcc gccttcggcc tcgggggaac ccccttccc 900
204 ccccgcccc aggcctgat cgcgcctat accgccttg acgaggccat ggaagcctc 960
205 gcccgccgt cgcagcctt aaacctggag ttggccctcc tggaggcggg aaggccctg 1020
206 gccgcggagg cctacccca gccacgggc gctccttccc cagaggtcgg ccccaagccg 1080
207 gaaagcccc cyaccggga cccccaagg cccgaggagg cgcgcgacct gcgggagcgg 1140
208 tggcgggcct tctcgaggc cctcaggccc accctacggg ccttcgtgcy ggaagcccg 1200
209 cggaggttcc ggaagggca gctctgctc gctttccccc aggacaaggc ctccactac 1260
210 cgcaaggcct cggaaacagaa ggtgaggctc ctcgccctgg ccagggccca ttccgggtg 1320
211 gaggaggtcg tctctgctt ggaaggagaa aaaaaagcc tgagcccaag gcccggccc 1380
212 gccccacctc ctgaagcgc cgcacccccc ggcctctccc aggaggaggt agagggcgg 1440
213 aaagcggcgg aggaagcccc ggaaggaggc ttgaggcggg tggtcgcct cctgggggg 1500
214 cgggtgctct ggtgctggcg gccagagacc cgggagggc cggaggaggga acccctgagc 1560
215 caagacgaga tagggggtac tggatatata 1590
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 464
220 <212> TYPE: PRT
221 <213> ORGANISM: Thermus thermophilus
223 <400> SEQUENCE: 4
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225 1 5 10 15
227 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
228 20 25 30
230 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
231 35 40 45
233 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
234 50 55 60
236 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
237 65 70 75 80
239 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
240 85 90 95
242 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
243 100 105 110
245 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
246 115 120 125
248 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Pro Pro Pro
249 130 135 140
251 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
252 145 150 155 160
254 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
255 165 170 175
257 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
258 180 185 190
260 Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
261 195 200 205

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Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

263 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 264 210 215 220
 266 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 267 225 230 235 240
 269 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 270 245 250 255
 272 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 273 260 265 270
 275 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 276 275 280 285
 278 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 279 290 295 300
 281 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 282 305 310 315 320
 284 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 285 325 330 335
 287 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 288 340 345 350
 290 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 291 355 360 365
 293 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 294 370 375 380
 296 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 297 385 390 395 400
 299 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 300 405 410 415
 302 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 303 420 425 430
 305 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 306 435 440 445
 308 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 309 450 455 460
 315 <210> SEQ ID NO: 5
 316 <211> LENGTH: 454
 317 <212> TYPE: PRT
 318 <213> ORGANISM: Thermus thermophilus
 320 <400> SEQUENCE: 5
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 322 1 5 10 15
 324 Val Gly Gln Glu His Val Lys Glu Pro Leu Lys Ala Ile Arg Glu
 325 20 25 30
 327 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 328 35 40 45
 330 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 331 50 55 60
 333 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 334 65 70 75 80
 336 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 337 85 90 95

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6

<210> 89
<211> 182
<212> PRT
<213> Deinococcus radiodurans

<400> 89

Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
1 5 10 15

Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
20 25 30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
35 40 45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
50 55 60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala (Xaa) Lys
65 70 75 80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
85 90 95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
100 105 110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
115 120 125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
130 135 140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
145 150 155 160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
165 170 175

Glu Leu Leu Gly Glu Arg
180

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all item 10
on Enva
summary
sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000
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Input Set : A:\R10301.app
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L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:552 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:552 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:552 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:1062 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1062 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
L:1074 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1074 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1074 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1506 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:66
L:1506 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:1506 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
L:1519 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67
L:1519 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67
L:1519 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:67
L:1532 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68
L:1532 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68
L:1532 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:68
L:2169 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:89
L:2169 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:89
L:2252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
L:2252 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
M:340 Repeated in SeqNo=91

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